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#2

RAW SEQUENCE LISTING DATE: 09/20/2001 PATENT APPLICATION: US/09/944,930 TIME: 13:58:04

Input Set : A:\PP16021.002 SEQLIST.TXT
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4 <110> APPLICANT: Hageman, Robert V.
              Shirley, Bret A.
              Bajwa, Kamaljit K.
      8 <120> TITLE OF INVENTION: Stabilized FGF Formulations Containing
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     11 <130> FILE REFERENCE: PP16021.002
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                                                             30
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59 35 45 40 60 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser 61 50 55 62 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly 63 65 70 75 80 64 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Glu 65 85 90 66 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser 67 100 · 110 105 68 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro 69 115 120 125 70 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala 130 71 135 140 72 Lys Ser 73 145 76 <210> SEQ ID NO: 3 77 <211> LENGTH: 155 78 <212> TYPE: PRT 79 <213> ORGANISM: Homo sapiens 81 <400> SEQUENCE: 3 82 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly 83 10 84 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu 85 20 86 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg 87 35 40 88 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu 89 55 50 90 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn 70 92 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys 93 85 90 95 94 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr 95 100 105 110 96 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys 97 115 120 125 98 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys 130 99 135 100 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 101 145 150 155 104 <210> SEQ ID NO: 4 105 <211> LENGTH: 155 106 <212> TYPE: PRT 107 <213> ORGANISM: Bos taurus 109 <400> SEQUENCE: 4 110 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly 111 1 112 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu 113 20 25 30

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119 120	Arg	Tyr	Leu	Ala	Met	70 Lys	Glu	Asp	Gly	Arg	75 Leu	Leu	Ala	Ser	Lys	80 Cys		
121		шhт	3	<i>α</i> 1	85	Dh a	Dh -	Dha	Q1	90	T	a 1	G	3	95			
123	Val	THE	Asp	100	Cys	Pne	Pne	Pne	105	Arg	Leu	GIU	ser	110	Asn	Tyr		
124 125	Asn	Thr	Tyr 115	Arg	Ser	Arg	Lys	Tyr 120	Ser	Ser	Trp	Tyr	Val 125	Ala	Leu	Lys		
126	Arg	Thr	Gly	Gln	Tyr	Lys	Leu	Gly	Pro	Lys	Thr	Gly	Pro	Gly	Gln	Lys		
127	_	130		_			135					140						
	Ala	Ile	Leu	Phe	Leu		Met	Ser	Ala	Lys								
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	ttc Phe								_							_	96	
148	1110	Lys	nsp	20	цуз	пту	шeu	1 7 1	25	пур	non	СТУ	ату	30	FIIC	шец		
	cgc	atc	cac		gac	aac	cga	att		aaa	atc	caa	σaσ		aσc	gac	144	
	Arg						-	_	_		_			_	_	-		
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	Pro		Ile	Lys	Leu	Gln	Leu	Gln	Ala	Glu	Glu	Arg	Gly	Val	Val	Ser		
156		50					55	_	_		_	60						
	atc											_	-	-	_		240	
160	Ile 65	ьуѕ	СТА	Val	Cys	70	ASII	Arg	Tyr	Leu	A1a 75	мет	ràs	GIU	Asp	-		
	aga	tta	cta	act	tct		tat	att	aca	αat	• –	tat	ttc	+++	+++	80 gaa	288	
	Arg																200	
164	5				85	-10		, 4.2		90	014	0,0	1 110	1 110	95	O L u		
166	cga	ttg	gaa	tct	aat	aac	tac	aat	act	tac	cgg	tca	agg	aaa	tac	acc	336	
	Arg																	
168		-		100					105				_	110	_			
	agt																384	
	Ser	Trp		Val	Ala	Leu	Lys		Thr	Gly	Gln	Tyr		Leu	Gly	Ser		
172	.	.	115	a 1				120					125	_ •		_ *		
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	Pro	_			_	_					_						40
195			Dou	110	5	op	011		DCI	10	1114	1 110	110	110	15	1120	
	ttc	aaa	qat	cca	aaa	cqa	cta	tat	tat		aac	aaa	aaa	ttc		cta	96
	Phe								-								
199		-	-	20	-	_		_	25	-		-	-	30			
201	cga	atc	cac	cca	gat	ggg	cga	gta	gat	ggg	gta	cga	gaa	aaa	tcc	gat	144
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	Pro		Ile	Lys	Leu	Gln		Gln	Ala	Glu	Glu	_	Gly	Val	Val	Ser	
207	•	50		_			55					60					
	atc				_	_		_			•	_		_	_		240
	Ile	ьys	GTÀ	vaı	Cys		Asn	Arg	Tyr	Leu		Met	ьуs	GIu	Asp		
	65	at a	ata	~~~	+	70	+~+	~+ ·	200	~~+	75	+	++-	++-	++-	80	200
	cga Arg										_	_				_	288
215	AIG	цеu	пеп	Ата	85	пуэ	Cys	Val	1111	90	GIU	Cys	Pile	Pile	95	GIU	
	cga	cta	gaa	tee		aac	tat	aac	acc		cga	taa	сαа	aaa		tcc	336
	Arg		_								_		_				
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249 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu 250 20 26 27 26 28 26 26 26 26 26 26 26 26 26 26 26 26 26	249 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu 250			aσc	aac	acc		cca	CCC	αας	cac		ааσ	αac	CCC	aan		cta	96
250 20 25 25 30 30 144 255 30 30 144 255 37 72 25 25 36 37 29 37 29 37 29 37 37 29 37 37 29 37 37 37 37 37 37 37 3	25									_ _			_	_		_		_	70
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253 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg 254	253 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg 254		tac	tac	aaa		aaa	aac	ttc	ttc		cac	atc	cac	ccc		aac	cσa	144
254 gt gac ggg gtc cgg gag aaa gac gac ccc a cac aac caa cct acc atc aac cac c	254	_		·							_	_				_		-	
257	257		4	4	_			7									1	J	
257	257	256	gtt	gac	ggg	gtc	cqq	gag	aaq	aqc	gac	cct	cac	atc	aaq	cta	caa	ctt	192
258	258														_				
261 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn	261 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn 262 65 70 75 80 268 cgt tac ctg gct atg aag gaa gat gga aag tta ctg gct tct aaa tgt 288 265 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys 266 85 90 90				_		_		_		-				-				
262 65	262 65	260	caa	gca	gaa	gag	aga	gga	gtt	gtg	tct	atc	aaa	gga	gtg	tgt	gct	aac	240
288	264 cgt tac ctg gct atg aag gaa gat gga aga tta ctg gct tct aaa tgt 288 265 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys 95 266	261	Gln	Ala	Glu	Glu	Arg	Gly	Val	Val	Ser	Ile	Lys	Gly	Val	Cys	Ala	Asn	•
265 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys 85	265 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys 95 266 85 90 95 95 268 gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac 336 269 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr 110 272 aat act tac cgg tca agg aaa tac acc agt tgg tat gtg gca ctg aaa 384 273 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys 125 274 115 120 125 275 cga act ggg cag tat aaa ctt gga tcc aaa aca aca agg cct ggg cag aaa 432 277 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys 130 135 280 gct ata ctt ttt ctt cca atg tc gct aag agc tg tg 140 gag cct gag aaa 468 281 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser * 155 285 <210 > SEQ ID NO: 8 286 <211 > LENGTH: 468 287 <212 > TYPE: DNA 288 <213 > ORGANISM: Bos taurus 290 <220 > FEATURE: 910	262	65					70					75					80	
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268 gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac 336	268 gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac 2669 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr 100 100 105 110 110 110 110 110 110 110	265	Arg	Tyr	Leu	Ala	Met	Lys	Glu	Asp	Gly	Arg	Leu	Leu	Ala	Ser	Lys	Cys	
269 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr 100	269 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr 100	266					85					90					95		
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274	274											_				-	_		384
276 cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct ggg cag aaa 432 277 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys 278	276 cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct ggg cag aaa		Asn	Thr		Arg	Ser	Arg	Lys	Tyr	Thr	Ser	Trp	Tyr	Val	Ala	Leu	Lys	
277 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys 278	277 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys 278																		
278	278					-											_		432
280 gct ata ctt ttt ctt cca atg tct gct aag agc tga 468 281 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser * 282 145	280 gct ata ctt ttt ctt cca atg tct gct aag agc tga 468 281 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser * 282 145 150 150 155 285 <210> SEQ ID NO: 8 286 <211> LENGTH: 468 287 <212> TYPE: DNA 288 <213> ORGANISM: Bos taurus 290 <220> FEATURE: 291 <221> NAME/KEY: CDS 292 <222> LOCATION: (1)(468) 294 <400> SEQUENCE: 8 295 atg gca gcc ggg agc atc acc acg ctg cca gcc cta cca gaa gat ggg 48 296 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly 297 1 5 10 15 299 ggg tcc ggg gcc ttc cca cca ggg cac ttc aaa gat cca aaa cga cta 96 300 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu 301 20 25 30 303 tat tgt aaa aac ggg ggg ttc ttc cta cga atc cac cac gat ggg cga 144 304 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg		Arg		GLy	GIn	Tyr	Lys		Gly	Ser	Lys	Thr	_	Pro	Gly	Gln	Lys	
281 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser * 282 145	281 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser * 282 145						_ 4. 4.												4.50
282 145	282 145		-						_		_	_	_	_					468
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/944,930

DATE: 09/20/2001 TIME: 13:58:05

Input Set : A:\PP16021.002 SEQLIST.TXT
Output Set: N:\CRF3\09202001\1944930.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date